



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/803,459  
Source: IFW  
Date Processed by STIC: 3/26/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

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## Raw Sequence Listing Error Summary

| ERROR DETECTED   | SUGGESTED CORRECTION  | SERIAL NUMBER: <u>10/803,459</u> |
|--|---|----------------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |   |                                  |
| 1 _____ Wrapped Nucleics<br>Wrapped Aminos   | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."  |                                  |
| 2 _____ Invalid Line Length  | The rules require that a line not exceed 72 characters in length. This includes white spaces.   |                                  |
| 3 _____ Misaligned Amino<br>Numbering  | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.   |                                  |
| 4 _____ Non-ASCII  | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.  |                                  |
| 5 _____ Variable Length  | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  |                                  |
| 6 _____ PatentIn 2.0<br>"bug"  | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.   |                                  |
| 7 _____ Skipped Sequences<br>(OLD RULES)   | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |                                  |
| 8 _____ Skipped Sequences<br>(NEW RULES)   | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000  |                                  |
| 9 _____ Use of n's or Xaa's<br>(NEW RULES)   | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.  |                                  |
| 10 _____ Invalid <213><br>Response   | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence   |                                  |
| 11 _____ Use of <220>  | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)  |                                  |
| 12 _____ PatentIn 2.0<br>"bug"   | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.   |                                  |
| 13 _____ Misuse of n/Xaa   | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid  |                                  |



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,459

DATE: 03/26/2004

TIME: 07:27:09

Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

3 <110> APPLICANT: Gertler, Arie  
4 Krishna, Radha G.  
6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO  
8 <130> FILE REFERENCE: 28758.1  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/803,459  
C--> 10 <141> CURRENT FILING DATE: 2004-03-19  
10 <160> NUMBER OF SEQ ID NOS: 8  
12 <170> SOFTWARE: PatentIn version 3.2  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 630  
16 <212> TYPE: DNA  
17 <213> ORGANISM: human leptin receptor binding domain  
20 <220> FEATURE:  
21 <221> NAME/KEY: CDS  
22 <222> LOCATION: (1)..(630)  
24 <220> FEATURE:  
25 <221> NAME/KEY: misc\_feature  
26 <222> LOCATION: (6)..(6)  
27 <223> OTHER INFORMATION: n is a, c, g, or t  
29 <400> SEQUENCE: 1  
30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac 48  
31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr  
32 1 5 10 15  
34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt 96  
35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu  
36 20 25 30  
38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt 144  
39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys  
40 35 40 45  
42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat 192  
43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr  
44 50 55 60  
46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta 240  
47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu  
48 65 70 75 80  
50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca 288  
51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser  
52 85 90 95  
54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca 336  
55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro  
56 100 105 110  
58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta 384  
59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu

Does Not Comply  
Corrected Diskette Needed  
p.3

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,459

DATE: 03/26/2004

TIME: 07:27:09

Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

```
60          115          120          125          432
62 ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa
63 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
64          130          135          140          480
66 ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg
67 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
68 145          150          155          160          528
70 tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca
71 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
72          165          170          175          576
74 gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat
75 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
76          180          185          190          624
78 gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc
79 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
80          195          200          205          630
82 atg gat
83 Met Asp
84          210
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 210
89 <212> TYPE: PRT
90 <213> ORGANISM: human leptin receptor binding domain
92 <400> SEQUENCE: 2
94 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
95 1          5          10          15
98 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
99          20          25          30
102 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
103          35          40          45
106 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
107          50          55          60
110 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
111 65          70          75          80
114 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
115          85          90          95
118 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
119          100          105          110
122 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
123          115          120          125
126 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
127          130          135          140
130 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
131 145          150          155          160
134 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
135          165          170          175
138 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
139          180          185          190
142 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,459

DATE: 03/26/2004

TIME: 07:27:09

Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

```

143          195          200          205
146 Met Asp
147      210
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 36
152 <212> TYPE: DNA
153 <213> ORGANISM: synthetic
155 <400> SEQUENCE: 3
156 ggaattccat atgattgatg tcaatatcaa tatctc
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 39
161 <212> TYPE: DNA
162 <213> ORGANISM: synthetic
164 <400> SEQUENCE: 4
165 cataggaagc ttccaatcca tgacaactgt gtaggctgg
168 <210> SEQ ID NO: 5
169 <211> LENGTH: 12
170 <212> TYPE: PRT
171 <213> ORGANISM: human leptin receptor fragment
174 <220> FEATURE:
175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (1)..(11)
177 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid.
179 <400> SEQUENCE: 5
> 181 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu
182 1          5          10
185 <210> SEQ ID NO: 6
186 <211> LENGTH: 5
187 <212> TYPE: PRT
188 <213> ORGANISM: Consensus
191 <220> FEATURE:
192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (3)..(3)
194 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
196 <400> SEQUENCE: 6
> 198 Trp Ser Xaa Trp Ser
199 1          5
202 <210> SEQ ID NO: 7
203 <211> LENGTH: 627
204 <212> TYPE: DNA
205 <213> ORGANISM: chicken leptin receptor binding domain
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)..(627)
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: (6)..(6)
215 <223> OTHER INFORMATION: n is a, c, g, or t
217 <400> SEQUENCE: 7

```

*invalid <213> response. See item 10 on Error Summary Sheet.*

*invalid*

*invalid*

## RAW SEQUENCE LISTING

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Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

```

--> 218 atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac      48
    219 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
    220 1          5          10          15
    222 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc.      96
    223 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
    224          20          25          30
    226 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt      144
    227 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
    228          35          40          45
    230 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat      192
    231 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
    232          50          55          60
    234 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt      240
    235 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
    236 65          70          75          80
    238 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca      288
    239 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
    240          85          90          95
    242 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca      336
    243 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
    244          100          105          110
    246 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg      384
    247 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
    248          115          120          125
    250 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag.      432
    251 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
    252          130          135          140
    254 ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg      480
    255 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
    256 145          150          155          160
    258 tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa      528
    259 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
    260          165          170          175
    262 ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc      576
    263 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
    264          180          185          190
    266 tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa      624
    267 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
    268          195          200          205
    270 gat
    271 Asp
    275 <210> SEQ ID NO: 8
    276 <211> LENGTH: 209
    277 <212> TYPE: PRT
    278 <213> ORGANISM: chicken leptin receptor binding domain
    280 <400> SEQUENCE: 8
    282 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
    283 1          5          10          15
    286 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu

```

## RAW SEQUENCE LISTING

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Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

```

287          20          25          30
290 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
291          35          40          45
294 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
295          50          55          60
298 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
299 65          70          75          80
302 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
303          85          90          95
306 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
307          100          105          110
310 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
311          115          120          125
314 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
315          130          135          140
318 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
319 145          150          155          160
322 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
323          165          170          175
326 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
327          180          185          190
330 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
331          195          200          205
334 Asp

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/803,459

DATE: 03/26/2004  
TIME: 07:27:10

Input Set : D:\28758.txt  
Output Set: N:\CRF4\03262004\J803459.raw

Please Note:

se of n and/or Xaa have been detected in the Sequence Listing. Please review the  
equence Listing to ensure that a corresponding explanation is presented in the <220>  
o <223> fields of each sequence which presents at least one n or Xaa.

eq#:1; N Pos. 6/  
eq#:5; Xaa Pos. 41  
eq#:6; Xaa Pos. 3/  
eq#:7; N Pos. 6)



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/803,459

DATE: 03/26/2004

TIME: 07:27:10

Input Set : D:\28758.txt

Output Set: N:\CRF4\03262004\J803459.raw

.:10 M:270 C: Current Application Number differs, Replaced Current Application No  
.:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
.:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
.:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
.:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
.:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

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